

### Amendments to the Specification

Please replace the paragraph at page 1, beginning with line 10 with the following:

a<sub>1</sub> This application claims the benefit of U.S. Provisional Application No. 60/135,391 filed May 21, 1999, U.S. Provisional Application No. 60/092,936 filed July, 15 1998, U.S. Application No. 09/352,168 filed July 12, 1999, now issued U.S. Patent Number 6,211,434 and is a Continuation of U.S. Application No. 09/352,159 filed July 12, 1999, now issued U.S. Patent Number 6,211,435 all of which are hereby incorporated by reference.

[ Please replace the paragraph at page 59, beginning at line 15 with the following: ]

a<sub>2</sub> The amine oxidase domain of trAPO contains several key features shared by this class of enzymes, including an amino-terminal dinucleotide (ADP) binding region characterized by a beta-alpha-beta stretch containing three invariant glycines (G -X-G-X-X-G) in the beta-alpha turn. In trAPO, this sequence is (DVVVVGAGLSG) (SEQ ID NO: 54). This region is involved in FAD binding. Absent are several features unique to the mammalian amine oxidases, including several essential cysteine residues (Wu *et al.*, *Mol Pharm* 43:888 (1993)), one of which (Cys-406 of MAO-A) is involved in covalent binding of FAD, and a carboxy-terminal extension that has been demonstrated to be involved in transporting to and anchoring the MAO in the outer mitochondrial membrane. The *Aspergillus* enzyme MAO-N has been demonstrated to contain non-covalent FAD, and also lacks the conserved cysteine. Therefore it is possible that the APO enzyme has a non-covalent FAD. The *Aspergillus* MAO-N has a carboxy-terminal tripeptide Ala-Arg-Leu that is involved in peroxisomal targeting and localization; this sequence is absent from *Exophiala* MAO.

[ Please replace the paragraph at page 68, beginning at line 25 with the following: ]

a<sub>3</sub> Preliminary sequence results were entered into GCG, and nucleotide and protein alignments were done in a pileup using a software program called Genedoc for shading and homology comparisons (Nicholas, *et al.*, *EMBNEW.NEWS* 4:14 (1997); or at the Internet site <http://www.cris.com/~Ketchup/genedoc.shtml> ~~www.cris.com/~Ketchup/genedoc.shtml~~). The



first APAO (SEQ ID NO: 22) sequences were included for comparison. Comparing the reference sequence SEQ ID NO: 22 to the other homologs sequence identities range from 96 to 99% (identities are lower since APAO introns were not included). Homologies are slightly higher comparing *Exophiala* genes sequences. At the amino acid sequence level the comparison of the reference sequence (SEQ ID NO: 23) to the other homologs yielded sequence identities of approximately 97%.

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